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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-071-879-9-inv.res made by jdelaval on Wed 1 Dec 104 15:41:41-PST.

Query sequence being compared: US-10-071-879-9' (1-1908)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-071-879-9' (1-1908) with:
File : ac018798.seq

100-
N -
U -
M -
B -
E -
R -
O -
F -
S -
E -
U -
U -
C -
C -
E -
S -
SCORE 0 128 255 383 511 638 766 894 1021 1149
STDDEV

1 NUERSE
comp.

PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 1.00 Window size 32
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
1149 0 0.00

Times: CPU Total Elapsed
00:00:00.95 00:00:01.00

Number of residues: 180153
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. ac018798	TOIG of: ac018798	check: 176	180153	1149	1597	0.00 0

1. US-10-071-879-9' (1-1908)
TOIG of: ac018798 check: 1761 from: 1 to: 18015

TOIG of: ac018798 check: 1761 from: 1 to: 180153

LOCUS AC018798 180153 bp DNA linear HTG 17-AUG-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-15u8, WORKING DRAFT SEQUENCE,
22 unordered pieces.
ACCESSION AC018798
VERSION AC018798.7 GI:9838037
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 180153)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 180153)
Waterston, R.H.
Direct Submission
Submitted (19-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:8567925.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project information
Center project name: H NH0015108
----- Summary Statistics -----
Sequencing vector: M13, 864
Sequencing vector: plasmid, 144
Chemistry: Dye-terminator Big Dye, 144 of reads
Chemistry: Dye-terminator Big Dye, 144 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169308 bases at least Q40
Consensus quality: 174059 bases at least Q30
Consensus quality: 176629 bases at least Q20
Insert size: 171000; agarose-fp
Insert size: 179077; sum-of-ctigs
Quality coverage: 4.43 in Q20 bases; agarose-fp
Quality coverage: 4.28 in Q20 bases; sum-of-ctigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1756: contig of 1756 bp in length
1757 1856: gap of unknown length
1857 3442: contig of 1586 bp in length
3443 3543: gap of unknown length
3543 6427: contig of 2885 bp in length
6427 6428: gap of unknown length
6428 9099: contig of 2472 bp in length
9099 9100: gap of unknown length
9100 10529: contig of 1430 bp in length
10529 10530: gap of unknown length
10530 14118: contig of 3489 bp in length
14118 14119: gap of unknown length

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1000 1010 1020 1030 1040 1050 1060
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1070 1080 1090 1100 1110 1120 1130
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1140 1150 1160 1170 1180 1190 1200 1210
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1360 1370 1380 1390 1400 1410 1420
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1500 1510 1520 1530 1540 1550 1560 1570
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1580 1590 1600 1610 1620 1630 1640
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NN
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 NNN
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12780 12790 12800 12810 12820 12830 12840
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> O <
O | O Intell:Genetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-071-879-9.res made by jdelaval on Wed 1 Dec 104 15:40:25-EST.

Query sequence being compared: US-10-071-879-9 (1-1908)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-071-879-9 (1-1908) with:
File : ac018798.seq

```

100-
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M -
B -
E -
R -
O -
F -10-
S -
E -5-
O -
U -
N -
C -
E -
S -0-
SCORE 0 15 30 44 59 74 89 103 118 133
STDDEV
PARAMETERS
Similarity matrix      Unitary      K-tuple
Mismatch penalty      1          Joining penalty
Gap penalty            1.00       Window size
Gap size penalty       0.33
Cutoff score           0
Randomization group    0

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SEARCH STATISTICS

Scores: Mean Median Standard Deviation
133 0 0.00
Times: CPU Total Elapsed
00:00:00.05 00:00:01.00

Number of residues: 180153
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. ac018798	TOIG of: ac018798	check: 176	180153	133	763	0.00 0
1. US-10-071-879-9 (1-1908)						
ac018798	TOIG of: ac018798	check: 1761	from: 1	to: 18015		
TOIG of: ac018798 check: 1761 from: 1 to: 180153						
LOCUS	AC018798	180153 bp	DNA	linear	HTG 17-AUG-2000	
DEFINITION	Homo sapiens chromosome 11 clone RP11-15L8, WORKING DRAFT SEQUENCE,					
ACCESSION	AC018798					
VERSION	AC018798.7 GI:9838037					
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Waterston, R.H.					
AUTHORS	The sequence of Homo sapiens clone					
TITLE	Unpublished					
JOURNAL	2 (bases 1 to 180153)					
REFERENCE	Waterston, R.H.					
AUTHORS	Submitted (19-DEC-1999) Genome Sequencing Center, Washington					
TITLE	University School of Medicine, 4444 Forest Park Parkway, St. Louis,					
JOURNAL	MO 63108, USA					
COMMENT	On Aug 17, 2000 this sequence version replaced gi:8567925.					

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H NH0015108
Summary Statistics
Sequencing vector: M13; 864
Sequencing vector: plasmid; 144
Chemistry: Dye-terminator Big Dye; 144 of reads
Chemistry: Dye-terminator Big Dye; 144 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169308 bases at least Q40
Consensus quality: 174059 bases at least Q30
Consensus quality: 176629 bases at least Q20
Insert size: 171000; agarose-fp
Insert size: 179077; sum-of-contigs
Quality coverage: 4.43 in Q20 bases; agarose-fp
Quality coverage: 4.28 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
* 1757: contig of 1756 bp in length
* 1856: gap of unknown length
* 1857: contig of 1586 bp in length
* 3442: gap of unknown length
* 3443: contig of 2885 bp in length
* 3543: gap of unknown length
* 6427: contig of 2472 bp in length
* 6428: gap of unknown length
* 6528: contig of 2472 bp in length
* 8999: gap of unknown length
* 9000: contig of 1430 bp in length
* 10529: gap of unknown length
* 10530: contig of 3489 bp in length
* 10630: gap of unknown length
* 14118: contig of 3489 bp in length
* 14119: gap of unknown length

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[illegible]

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42780	42790	42800	42810	42820	42830	42840
42850	42860	42870	42880	42890	42900	42910
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43130	43140	43150	43160	43170	43180	43190
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CGCCTGTATCCGACCTTTGGAGGGCTAAAGTGGGTGATCACCTGAGGTCAGAGATTCAAGACTAGCCT	44460	44470	44480	44490	44500	44510	44520
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